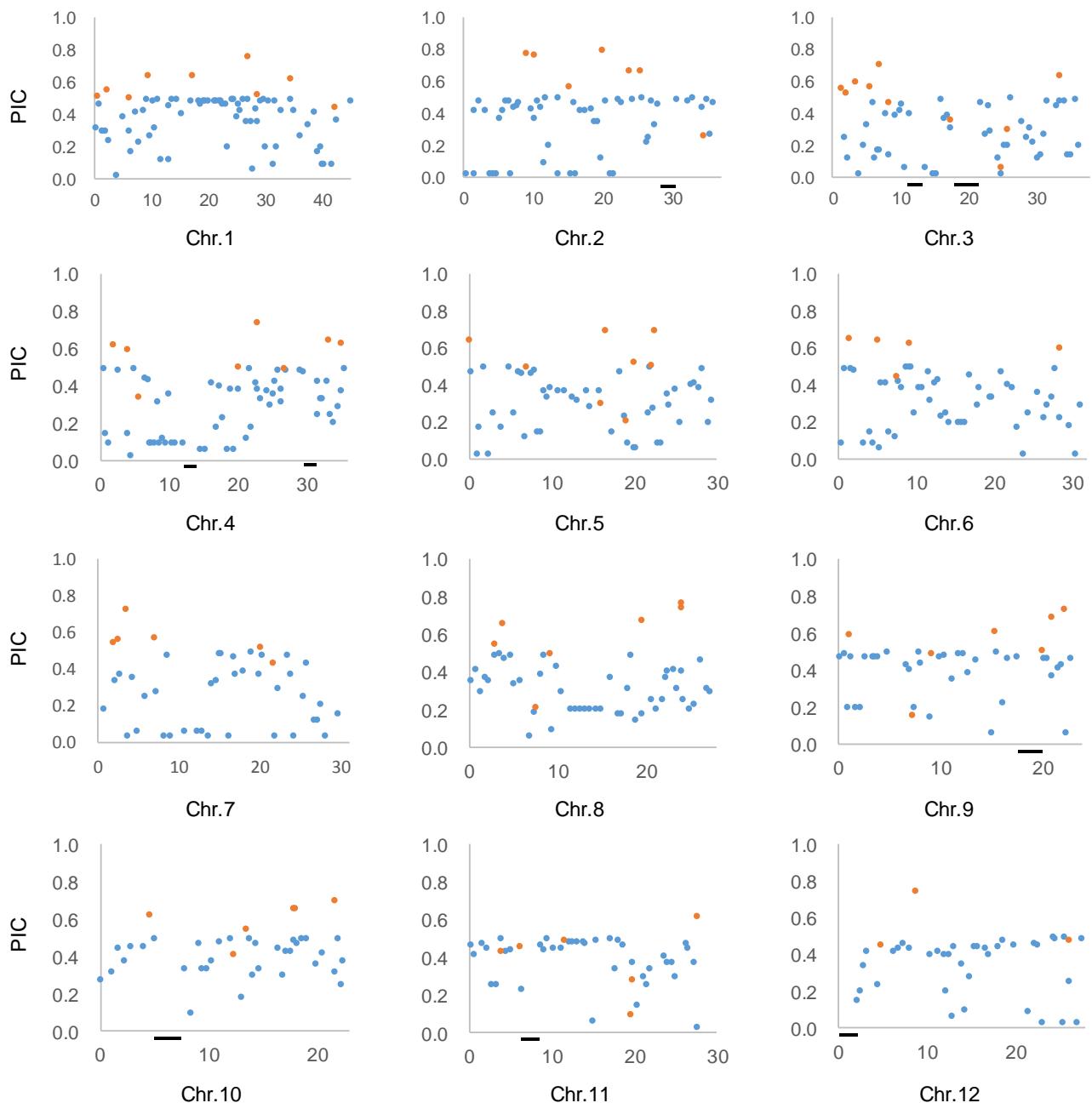


Supplemental Fig. 1

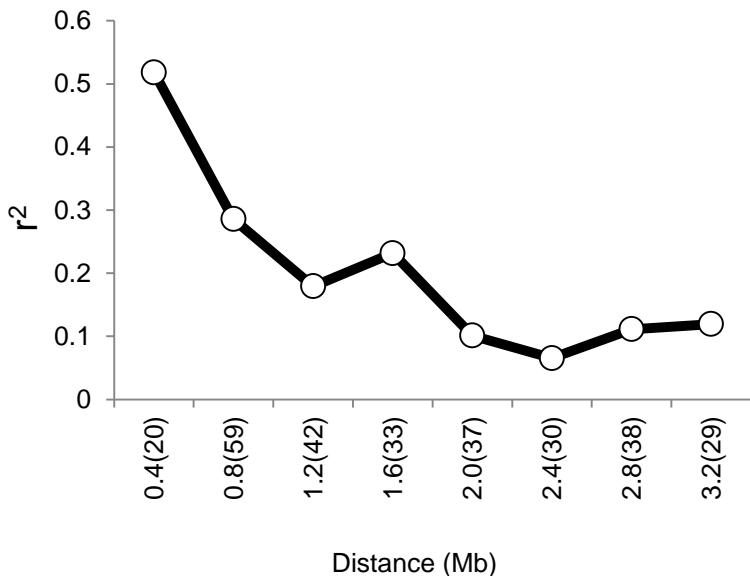
**Supplemental Fig.1.** The pedigree of cultivars in the advanced panel (AP) The AP consisted of 13 rice cultivars shown in gray boxes. These cultivars are in the pedigree of or an ancestor of Kitaake (shown in red).



**Supplemental Fig. 2. Polymorphic Information Content (PIC) values of single nucleotide polymorphisms (SNP: blue color) or simple sequence repeat (SSR: orange color) markers used in this study in the Hokkaido Rice Core panel (HRCP)**

The x-axes shows the marker position in each chromosome. The y-axes shows PIC values for each SNP or SSR marker. Horizontal lines show regions with no polymorphism markers for 2 Mb.

## Supplemental Fig. 2



**Supplemental Fig. 3. Median values of the estimate of linkage disequilibrium ( $r^2$ ) between SNP pairs within a 3200-kb distance on all 12 rice chromosomes.** The median  $r^2$  was calculated using 400-kb distances. The number in parentheses is the number of SNPs pair using calculation of  $r^2$  in each distance. SNPs pair with similar PIC value was used for calculation.